

ATAC-seq significance analysis

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An abbreviated version of this protocol was published in Science Advances in Feb 2020

Chromatin accessibility analysis reveals regulatory dynamics of developing human retina and hiPSC-derived retinal organoids

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Detailed protocol

1. Use ATAC-pipe(Zuqi Zuo et.al, *Briefings in Bioinformatics*, 2018) or other methods to get the differential peaks between groups, ranking the peak list using clustering, namely Sample.peakOrder.bed, and get the number of peaks in each groups, namely Sample.peakOrder.txt
2. Use ATAC-pipe to calculate the ATAC signal of each site on the genome of different groups of samples, that is, the file: Sample_pe.q10.sort.rmdup.shift.bedGraph
3. Use s011_chipSeq_intensity_fast2_p1.pl to calculate the ATAC signal value of 1kb on the left and right of the summit of each peak, that is: the heatmap.txt file
4. Use s011_heatmap2_p2.py to plot the heatmap.

Related files



Code.zip



How to cite:(Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. zhang, w. (2021). ATAC-seq significance analysis. Bio-protocol Preprint. bio-protocol.org/prep798.
2. Xie, H., Zhang, W., Zhang, M., Akhtar, T., Li, Y., Yi, W., Sun, X., Zuo, Z., Wei, M., Fang, X., Yao, Z., Dong, K., Zhong, S., Liu, Q., Shen, Y., Wu, Q., Wang, X., Zhao, H., Bao, J., Qu, K. and Xue, T.(2020). Chromatin accessibility analysis reveals regulatory dynamics of developing human retina and hiPSC-derived retinal organoids . Science Advances 6(6). DOI: [10.1126/sciadv.aay5247](https://doi.org/10.1126/sciadv.aay5247)

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